Original Article

Genetic Analysis of Quantitative Traits Associated with Drought Tolerance Attributes in Rice RIL Populations Under Reproductive Moisture Stress

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Abstract

Rice productivity and yield stability are negatively affected by moisture stress, becoming a challenge to farming systems as the world's climate shifts. Drought is one of the primary factors limiting rice production in rainfed ecosystems during the reproductive phase. In the context of abiotic stress breeding, the finding of drought tolerant genotypes during the reproductive stage provides researchers with extra benefits in developing stable varieties for moisture stress. Two different parents, CT- 9993 and Samba Mashuri were utilized to develop recombinant inbred lines for evaluation of drought tolerance during the study. Findings of the study expressed that yield and yield-attributing parameters varied significantly for genetic correlation, heritability, genetic advancement, etc. among RILs and parental lines over stressed experiment. Result of genetic analysis identified several lines which can be further exploited in developing drought tolerant cultivars to get sustainable yield under reproductive stress condition in rice.

Key words: Correlation, Drought tolerance, Genetic advance, Heritability, Moisture stress, Rice, RIL, Variability, Yield.

INTRODUCTION

Rice productivity and yield stability are negatively affected by moisture stress, becoming a challenge to farming systems as the world's climate shifts. A minimal amount of moisture stress, particularly during the vegetative stage in rice, may have a substantial effect on grain yield. As a result, rice farmers consider drought a significant abiotic stressor. Consequently, it is liable for up to 15% of the decrease in Indian crop productivity (Gorantla et al., 2005). In the Southern part of Asia, > 20 million hectares are in danger from drought due to global warming (Manrique-Carpintero et al., 2016). As one of the significant constraints in production, yield decrease due to drought emerged as the most crucial source of climate-related hazards (Pandey et al., 2009). Significant rain-fed areas of eastern India's drought are screened for resilience mostly during the rainy season in selected locations (Verulkar et al., 2010). In eastern India and adjacent Nepal, there are 17 million hectares of rice fields that are threatened by drought (Huke et al., 1982). Moisture stress is linked to duration and frequency of water deficiencies. Water deficits may occur early in the growth season or at any point between blooming and grain filling. Drought stress retards leaf growth, tillering, and photosynthesis, and early senescence diminishes photosynthetic rate and leaf size. Under drought circumstances, these variables all contribute to a drop in grain production. In addition, water scarcity increases the generation of reactive oxygen species (ROS), which results in lipid peroxidation, protein denaturation, and nucleic acid degradation, all of which have significant effects on the general metabolism, so reducing grain yield. Both the vegetative and reproductive phases of rice are particularly vulnerable to drought. When drought stress interacts with irreversible reproductive processes, grain output plummets dramatically. The phenotypic expression, especially during the reproductive phase, is the primary regulator of grain yield in rain-fed lowland rice, and any effort to screen for drought resistance must take reproductive stage variation into consideration. Therefore, classification drought-resistant rice lines from a pool of RILs with different drought tolerance during the vegetative or reproductive phases might provide new insights for rice breeding (Bunnag et al., 2013). As a potential answer to this problem, a drought-resistant, high-yielding cultivar may be developed. The present investigation has been conducted with the aim of identifying suitable lines which can be exploited directly or indirectly for developing abiotic stress tolerant cultivars in connection to drought.

MATERIALS AND METHODS

The plant materials used under study included a 150 RIL population derived from CT 9993 ×Samba Mashuri were raised at Visva-Bharati from December 2018 to April 2021. CT9993 is an upland japonica type rice (Lanceras et al. 2004), was utilized as a drought-tolerant parent (Bunnag et al. 2013), and Samba Mashuri, lowland-adapted popular rice cultivar (Sandhu et al. 2018), was used as drought susceptible parent (Rani et al. 2013). Irrigation schedule was modified for dry season field analysis and artificial moisture stress was applied for inducing water stress in reproductive stage. No irrigation was provided for growth after 55 days of sowing and the stress cycle was repeated up to maturity and final harvest. Phenotypic data was recorded for different attributing quantitative characters.

RESULT

All aspects of genetic variability, heritability, and correlation were considered in the evaluation of mapping populations. The analysis of variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in the broad sense, and genetic advance as percentage of population mean (GAM%) (Selection intensity at the 5% level) were all approximated using proper statistical methods (Singh and Chaudhary, 1979). **(Table 1)**

Table 1: Statistical description of different phenotypic characteristics of Rice RILs during moisture stress.

	PH	***RL***	***NT***	***NP***	***GY***
Mean	80.50	16.07	3.55	2.45	12.35
Standard Deviation	8.52	4.25	1.15	0.71	3.53
Kurtosis	3.45	-1.09	1.45	-0.53	-0.65
Skewness	1.25	-0.45	0.75	0.24	-0.40
Minimum	65.50	2.15	1.80	0.39	4.40
Maximum	117.00	24.30	7.50	4.49	20.25
PCV	9.85	27.69	22.75	35.29	23.82
GCV	9.87	28.76	22.63	31.56	24.53
ECV	0.75	6.24	8.37	14.21	7.23
(h2) Broad sense	98.60	94.67	84.66	81.42	91.63
GA (5%)	17.25	8.72	1.63	1.35	5.35
GAM (5%)	21.25	54.39	39.30	56.55	45.75

Where, PCV= Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, ECV=Environmental coefficient of variation, h^2= Heritability (broad sense), GA (5%)=Genetic advance, GAM(5%)= Genetic advance as percent of mean.

The mean value for Plant height character was 80.50 cm, with a standard deviation of 8.52, a kurtosis of 3.45, and a skewness of 1.25. The range of measurements was from 65.50 cm to 117 cm. During the dry season, however, the values for PCV, GCV, and ECV were 9.85%, 9.87%, and 0.75%, respectively. The findings for Broad sense heritability (h^2) were reported to be 98.60 %, but the values for GA (5%) and GAM (5%) were 17.25% and 21.25%, respectively.

The mean Root length was 16.07 cm, with a standard variation of 4.25. The kurtosis value was determined to be -1.09, while the skewness value was -0.45. The values ranged between 2.15 cm and 24.30 cm. The value of heritability in the broad sense (h^2) was determined to be 94.67 %, with GA (5%) at 8.72% and GAM (5%) at 54.39%. PCV, GCV, and ECV were determined to be, respectively, 27.69%, 28.76%, and 6.24%.

According to the observations, the character No. of Tillers had a mean value of 3.55, a range of 1.80 to 7.50, a kurtosis value of 1.45, and a skewness value of 0.75. The standard deviation value was calculated to be 1.15. The calculated percentages for PCV, GCV, and ECV were 22.75%, 22.63%, and 8.37%, respectively. The heritability was discovered to be 84.66 %, with the GA (5%) value being 1.63 % and the GAM (5%) value being 39.30 %.

The lowest and maximum range that was recorded for the trait No. of Panicle was 0.39 to 4.49, with a mean value of 2.45 nos. The kurtosis and skewness values ended up being -0.53 and 0.24 respectively. Heritability was reported to have a value of 81.42%, whereas the value of GA (5%) was 1.35%, and the value of GAM (5%) was 56.55%. It was discovered that the PCV, GCV, and ECV variations came in at 35.29%, 31.56%, and 14.21% correspondingly.

A value of 12.35 g was found to be the mean value for grain yield with a range extending from a minimum of 4.40 to 20.25 g. It was determined that the values for the standard deviation, kurtosis, and skewness were each 3.53, -0.65, and -0.40 correspondingly. Heritability was determined to be 91.63%, with GCV coming in at 24.53%, PCV coming in at 23.82%, and GA (5%) coming in at 5.35%.

The examination of Pearson correlation for the various yield attributing parameters demonstrates how multiple characteristics were connected with one another in our research based on the mean data of field evaluation **[Table 2].** Result expressed that characteristics, such as Plant height, Root length , Number of tillers , Number of panicles were discovered to be positively significant to Grain yield , and these characters positively contributed to the overall grain yield. In addition, the trait Plant Height was observed as positively significant to Number of Panicle but non-significant to Root length and Number of tillers. Trait Root length expressed significant positive relationship with Number of tiller but non-significant to Number of panicles. It was discovered that Number of tillers had a considerable positive significant impact on Number of panicles and Grain yield.

Table 2: Correlation of different major yield attributing characteristics of Rice RILs during moisture stress.

	PH	***RL***	***NT***	***NP***	***GY***
PH	1				
RL	0.063NS	1			
NT	0.035NS	0.187**	1		
NP	0.132*	0.042NS	0.427**	1	
GY	0.187**	0.167**	0.143**	0.221**	1

Where, PH= Plant height, RL=Root length, NT=No. of tillers, NP=No. of panicle, GY=Grain yield.

DISCUSSION

Genetic variability parameters reveal the degree of variation within a group. The co-efficient of variation that is expressed at both the phenotypic and genotypic levels was utilised to compare the variability of various features. The degree of genetic variability, heritability, and genetic advancement of the desirable traits all contribute to the effectiveness of breeding programmes. Variability is required for the improvement of genetic material. The degree of genetic diversity between genotypes is determined by metrics such as genotypic and phenotypic coefficients of variation.

The analysis of variance revealed very significant differences between genotypes for all of the investigated features. The results clearly demonstrated that yield and yield components varied widely across the RILs examined. Thus, there is a great deal of room for the selection of suitable genotypes that satisfy the fundamental requirements of the product profile in rice genotypes to be bred with better adaptation to moisture stress. Ashvani et al., (1997); Verma et al., (2000); Rani et al., (2001); Yadav et al., (2011); Anis et al., (2016); Limbani et al., (2017); Kishore et al., (2018); all observed comparable variation for characteristics under water stress and non-stress. The phenotypic coefficient of variation was found to be bigger than the genotypic coefficient of variation (GCV) for the majority of traits studied which is in accordance with the findings of other research (Kahani et al., (2015); Nitya et al., (2020); Nitya et al., (2021); Srivastava et al., (2009); Kumar et al., (2017). A modest disparity between the GCV and PCV values indicates their minimal environmental influence and, consequently, the significance of genetic variables in the development of characteristics. For Grain yield, Number of panicles, Number of tillers, and root length, high GCV and PCV were observed, and similar results were also observed by Singh et al., (2006), Mustafa and Elsheikh (2007), Sawarkar and Senapati (2014), and Limbani et al. ,(2017) for grain yield per plant, unfilled grains per panicle, for total grains per panicle, grain yield per plot, number of grains per panicle, and panicle weight, Singh et al. (2015) reported the values. Tuhina khatun (2015) reported the number of grains per panicle and grain yield per plant, but Anis et al. (2016) reported the number of full grains per panicle and grain yield per plot. In this investigation, both PCV and GCV levels were observed to be greater under condition and it may be attributed to the full expression of genetic potential in conditions of stress.

The genetic and phenotypic correlation coefficients between all attributes were investigated. According to the correlation analysis conducted in this study, Plant height (0.187**), Root length (0.167**), Number of tillers (0.143**) and Number of panicles (0.221**) were significantly correlated to grain yield. Similar results have been observed by other studies at the phenotypic level (Pantuwan et al.,2002; Yang et al., 2002). This discovery explains the significant link between grain yield and yield-attributing traits, and comparable findings have been published earlier (Bhutta et al.,2019).

Despite the drought stress delivered to the parents and RILs throughout the screening method for physiological and agronomic traits, a highly significant positive connection was observed between root length and grain production. In the stressed experiment, the average root length was substantially longer than in the control experiment. A positive link between total water intake and root properties, such as deeper root length, demonstrates conclusively that a plant's root system is necessary for extracting water from deeper soil layers during drought stress. Gowda et al. (2011) discovered that a plant's deep root system in a dry environment was a result of its need to obtain water to maintain its tissues pliable.

The estimation of heritability in a wide sense revealed that all attributes were impacted by drought stress. According to Kumar et al., (2007), during drought stress the heritability of rice is lower than under irrigated conditions. Under drought stress, heritability varied from 80.52% to 99.76% (Table 1) in the broad sense. In this study, all attributes revealed increased heritability under conditions of drought stress. High heritability suggests that breeders can select superior genotypes based on phenotypic performance based on a high proportion of heritable variation (Karthikeyan et al., 2010). Similar to the coefficient of variance, if the variability in the studied population is great, an effective selection of the majority of breeding traits would be achievable, hence confirming a significant genetic advance (Abarshahr et al., 2011). Genetic progress is a valuable indicator of the expected improvement resulting from the selection of the optimal trait. Estimated genetic advance as a percentage of the mean was found moderate for grain yield, Number of panicles, Number of tillers and root length. For plant height, a low genetic advance as percentage of mean was observed. Heritability with genetic progress should be utilised to anticipate the selection of superior genotypes (Ali et al., 2002). In this work, strong estimates of heritability and genetic advance were achieved for different traits indicated that these variables can be exploited for selection-based upland rice development. High heritability and moderate genetic advance for grain yield and root length imply both additive and non-additive gene activity in its inheritance (Lakshmi et al., 2016). For Plant height, Grain yield, Number of tillers, and Number of panicles, we achieved relatively high GCV, PCV, heritability, and genetic advance and these traits might be transferred to offspring via hybridization, and phenotypic selection would be effective.

CONCLUSION

Globally, the reproductive stage of rice crops is severely harmed by drought, making the development of drought-tolerant cultivars an urgent necessity. The analysis of variance revealed substantial heterogeneity in grain yield and yield contributing traits among RILs. High variance and heritability were reported for the majority of characteristics in the population. Estimates of variability, correlation, and heritability, along with genetic advance as a percentage of the mean for grain yield and other yield attributing characters indicate that selection of these traits may be advantageous for increasing grain yield, and yield attributing characters may be included as selection criteria for developing drought-smart cultivars.

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Conflicts of Interest

The authors declare that they have no conflict of interest.

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